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Sequence Listing was accepted.

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Reviewer: Durreshwar Anjum

Timestamp: [year=2007; month=12; day=6; hr=11; min=27; sec=41; ms=538; ]

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Application No: 10759256 Version No: 2.0

**Input Set:**

**Output Set:**

**Started:** 2007-11-16 19:19:16.385  
**Finished:** 2007-11-16 19:19:18.648  
**Elapsed:** 0 hr(s) 0 min(s) 2 sec(s) 263 ms  
**Total Warnings:** 35  
**Total Errors:** 0  
**No. of SeqIDs Defined:** 35  
**Actual SeqID Count:** 35

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (1)
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
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W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
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W 213	Artificial or Unknown found in <213> in SEQ ID (9)
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W 213	Artificial or Unknown found in <213> in SEQ ID (13)
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W 213	Artificial or Unknown found in <213> in SEQ ID (19)
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**Input Set:**

**Output Set:**

**Started:** 2007-11-16 19:19:16.385  
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**Actual SeqID Count:** 35

Error code	Error Description
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SUBSTITUTE SEQUENCE LISTING

<110> Conseiller, Emmanuel  
Debussche, Laurent  
Gallagher, William

<120> Polypeptide (MBP1) Capable Of Interacting With Oncogenic Mutants Of The P53 Protein

<130> ST98033

<140> 10759256  
<141> 2004-01-20

<150> 09/829,936

<151> 2001-04-11

<150> FR9812754  
<151> 1998-10-12

<160> 35

<170> PatentIn version 3.3

<210> 1

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide 5'-1 (p53)

<400> 1

agatctgtat ggaggagccg cag

23

<210> 2

<211> 29

<212> DNA  
<213> Artificial Sequence  
<220>  
<223> Oligonucleotide 3' -393 (p53)

<400> 2  
agatctcatc agtctgagtc aggcccttc

29

<210> 3

<211> 15

<212> DNA

<213> Artificial Sequence

<220>  
<223> Oligonucleotide H175 3'

<400> 3  
ggggcagtgc ctcac

15

<210> 4

<211> 15

<212> DNA

<213> Artificial Sequence

<220>  
<223> Oligonucleotide W248 3'

<400> 4  
gggcctccag ttcat

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<210> 5

<211> 15

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide H273 3'

<400> 5

acaaacatgc acctc

15

<210> 6

<211> 15

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide G281 3'

<400> 6

gcgcccggcct ctccc

15

<210> 7

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide 5'-73

<400> 7

agatctgtgt ggccctgtca cca

23

<210> 8

<211> 1021

<212> DNA

<213> Artificial Sequence

<220>

<223> Murine MBP1 C-term fragment

<220>

<221> CDS

<222> (1)..(885)

<400> 8

tgc acc tgc cct gat ggt tac cga aaa att gga ccc gaa tgt gtg gac	48
Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro Glu Cys Val Asp	
1 5 10 15	
ata gat gag tgt cgt tac cgc tat tgc cag cat cga tgt gtg aac ctg	96
Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg Cys Val Asn Leu	
20 25 30	
ccg ggc tcc ttt cga tgc cag tgt gag cca ggc ttc cag ttg gga cct	144
Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe Gln Leu Gly Pro	
35 40 45	
aac aac cgc tct tgt gtg gat gtg aat gag tgt gac atg gga gcc cca	192
Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp Met Gly Ala Pro	
50 55 60	
tgt gag cag cgc tgc ttc aac tcc tat ggg acc ttc ctg tgt cgc tgt	240
Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe Leu Cys Arg Cys	
65 70 75 80	
aac cag ggc tat gag ctg cac cgg gat ggc ttc tcc tgc agc gat atc	288
Asn Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser Cys Ser Asp Ile	
85 90 95	
gat gag tgc ggc tac tcc agt tac ctc tgc cag tac cgc tgt gtc aac	336
Asp Glu Cys Gly Tyr Ser Ser Tyr Leu Cys Gln Tyr Arg Cys Val Asn	
100 105 110	
gag cca ggc cga ttc tcc tgt cac tgc cca caa ggc tac cag ctg ctg	384
Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly Tyr Gln Leu Leu	
115 120 125	
gct aca agg ctc tgc caa gat att gac gag tgt gaa aca ggt gca cac	432
Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu Thr Gly Ala His	
130 135 140	
caa tgt tct gag gcc caa acc tgt gtc aac ttc cat ggg ggt tac cgc	480
Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His Gly Gly Tyr Arg	
145 150 155 160	
tgt gtg gac acc aac cgt tgt gtg gag ccc tat gtc caa gtg tca gac	528
Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Val Gln Val Ser Asp	
165 170 175	
aac cgc tgc ctc tgc cct gcc tcc aat ccc ctt tgt cga gag cag cct	576
Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys Arg Glu Gln Pro	
180 185 190	
tca tcc att gtg cac cgc tac atg agc atc acc tca gag cga agt gtg	624
Ser Ser Ile Val His Arg Tyr Met Ser Ile Thr Ser Glu Arg Ser Val	
195 200 205	
cct gct gac gtg ttt cag atc cag gca acc tct gtc tac cct ggt gcc	672
Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val Tyr Pro Gly Ala	
210 215 220	

tac aat gcc ttt cag atc cgt tct gga aac aca cag ggg gac ttc tac 720  
Tyr Asn Ala Phe Gln Ile Arg Ser Gly Asn Thr Gln Gly Asp Phe Tyr  
225 230 235 240

att agg caa atc aac aat gtc agc gcc atg ctg gtc ctc gcc agg cca 768  
Ile Arg Gln Ile Asn Asn Val Ser Ala Met Leu Val Leu Ala Arg Pro  
245 250 255

gtg acg gga ccc cgg gag tac gtg ctg gac ctg gag atg gtc acc atg 816  
Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu Met Val Thr Met  
260 265 270

aat tcc ctt atg agc tac cgg gcc agc tct gta ctg aga ctc acg gtc 864  
Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val Leu Arg Leu Thr Val  
275 280 285

ttt gtg gga gcc tat acc ttc tgaagaccct cagggaaaggg ccatgtgggg 915  
Phe Val Gly Ala Tyr Thr Phe  
290 295

cccccttccc cctcccatag cttaagcagc cccgggggcc tagggatgac cgttctgctt 975

aaaggaacta tgatgtgaag gacaataaaag ggagaaaagaa ggaaaaa 1021

<210> 9

<211> 295

<212> PRT

<213> Artificial Sequence

<220>

<223> Murine MBP1 C-term fragment

<400> 9

Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro Glu Cys Val Asp  
1 5 10 15

Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg Cys Val Asn Leu  
20 25 30

Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe Gln Leu Gly Pro  
35 40 45

Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp Met Gly Ala Pro  
50 55 60

Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe Leu Cys Arg Cys  
65 70 75 80

Asn Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser Cys Ser Asp Ile  
85 90 95

Asp Glu Cys Gly Tyr Ser Ser Tyr Leu Cys Gln Tyr Arg Cys Val Asn  
100 105 110

Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly Tyr Gln Leu Leu  
115 120 125

Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu Thr Gly Ala His  
130 135 140

Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His Gly Gly Tyr Arg  
145 150 155 160

Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Val Gln Val Ser Asp  
165 170 175

Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys Arg Glu Gln Pro  
180 185 190

Ser Ser Ile Val His Arg Tyr Met Ser Ile Thr Ser Glu Arg Ser Val  
195 200 205

Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val Tyr Pro Gly Ala  
210 215 220

Tyr Asn Ala Phe Gln Ile Arg Ser Gly Asn Thr Gln Gly Asp Phe Tyr  
225 230 235 240

Ile Arg Gln Ile Asn Asn Val Ser Ala Met Leu Val Leu Ala Arg Pro  
245 250 255

Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu Met Val Thr Met  
260 265 270

Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val Leu Arg Leu Thr Val  
275 280 285

Phe Val Gly Ala Tyr Thr Phe

290

295

<210> 10

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide c-myc 5'

<400> 10

gatccatgga gcagaagctg atctccgagg aggacctga

39

<210> 11

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide c-myc 3'

<400> 11

gatctcaggc ctcctcgga gatcagcttc tgctccatg

39

<210> 12

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' MCS oligonucleotide

<400> 12

gatctcggtc gacctgcattt caattccccgg gtgcggccgc gagct

45

<210> 13

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> 3' MCS oligonucleotide

<400> 13

cgcggccgca cccgggaatt gcatgcaggt cgaccga

37

<210> 14

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide 3' mMBP1

<400> 14

cgttactggc agaggttaact gg

22

<210> 15

<211> 1513

<212> DNA

<213> Artificial Sequence

<220>

<223> MBP1 murine (complete sequence)

<220>

<221> CDS

<222> (49)..(1377)

<400> 15

gctgtggcag aaaccctga ctctgcccc ccacccccc gcctcagg atg ctc cct

Met Leu Pro

1

57

ttt gcc tcc tgc ctc ccc ggg tct ttg ctg ctc tgg gcg ttt ctg ctg  
Phe Ala Ser Cys Leu Pro Gly Ser Leu Leu Leu Trp Ala Phe Leu Leu

5

10

15

105

ttg ctc ttg gga gca gcg tcc cca cag gat ccc gag gag ccg gac agc  
Leu Leu Leu Gly Ala Ala Ser Pro Gln Asp Pro Glu Glu Pro Asp Ser

153

20	25	30	35
tac acg gaa tgc aca gat ggc tat gag tgg gat gca gac agc cag cac Tyr Thr Glu Cys Thr Asp Gly Tyr Glu Trp Asp Ala Asp Ser Gln His	40	45	50
tgc cgg gat gtc aac gag tgc ctg acc atc ccg gag gct tgc aag ggt Cys Arg Asp Val Asn Glu Cys Leu Thr Ile Pro Glu Ala Cys Lys Gly	55	60	65
gag atg aaa tgc atc aac cac tac ggg ggt tat ttg tgt ctg cct cgc Glu Met Lys Cys Ile Asn His Tyr Gly Tyr Leu Cys Leu Pro Arg	70	75	80
tct gct gcc gtc atc agt gat ctc cat ggt gaa gga cct cca ccg cca Ser Ala Ala Val Ile Ser Asp Leu His Gly Glu Gly Pro Pro Pro Pro	85	90	95
gcg gcc cat gct caa caa cca aac cct tgc ccg cag ggc tac gag cct Ala Ala His Ala Gln Gln Pro Asn Pro Cys Pro Gln Gly Tyr Glu Pro	100	105	110
gat gaa cag gag agc tgt gtg gat gtg gac gag tgt acc cag gct ttg Asp Glu Gln Glu Ser Cys Val Asp Val Asp Glu Cys Thr Gln Ala Leu	120	125	130
cat gac tgt cgc cct agt cag gac tgc cat aac ctt cct ggc tcc tac His Asp Cys Arg Pro Ser Gln Asp Cys His Asn Leu Pro Gly Ser Tyr	135	140	145
cag tgc acc tgc cct gat ggt tac cga aaa att gga ccc gaa tgt gtg Gln Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro Glu Cys Val	150	155	160
gac ata gat gag tgt cgt tac cgc tat tgc cag cat cga tgt gtg aac Asp Ile Asp Glu Cys Arg Tyr Arg Cys Gln His Arg Cys Val Asn	165	170	175
ctg ccg ggc tct ttt cga tgc cag tgt gag cca ggc ttc cag ttg gga Leu Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe Gln Leu Gly	180	185	190
cct aac aac cgc tct tgt gtq qat gtq aat gag tgt gac atq gga gcc Pro Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp Met Gly Ala	200	205	210
cca tgt gag cag cgc tgc ttc aac tcc tat ggg acc ttc ctg tgt cgc Pro Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe Leu Cys Arg	215	220	225
tgt aac cag ggc tat gag ctg cac cgg gat ggc ttc tcc tgc agc gat Cys Asn Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser Cys Ser Asp	230	235	240
atc gat gag tgc ggc tac tcc agt tac ctc tgc cag tac cgc tgt gtc Ile Asp Glu Cys Gly Tyr Ser Ser Tyr Leu Cys Gln Tyr Arg Cys Val	245	250	255

aac gag cca ggc cga ttc tcc tgt cac tgc cca caa ggc tac cag ctg			873
Asn Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly Tyr Gln Leu			
260	265	270	275
ctg gct aca agg ctc tgc caa gat att gac gag tgt gaa aca ggt gca			921
Leu Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu Thr Gly Ala			
280	285	290	
cac caa tgt tct gag gcc caa acc tgt gtc aac ttc cat ggg ggt tac			969
His Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His Gly Gly Tyr			
295	300	305	
cgc tgt gtg gac acc aac cgt tgt gtg gag ccc tat gtc caa gtg tca			1017
Arg Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Val Gln Val Ser			
310	315	320	
gac aac cgc tgc ctc tgc cct gcc tcc aat ccc ctt tgt cga gag cag			1065
Asp Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys Arg Glu Gln			
325	330	335	
cct tca tcc att gtg cac cgc tac atg agc atc acc tca gag cga agt			1113
Pro Ser Ser Ile Val His Arg Tyr Met Ser Ile Thr Ser Glu Arg Ser			
340	345	350	355
gtg cct gct gac gtg ttt cag atc cag gca acc tct gtc tac cct ggt			1161
Val Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val Tyr Pro Gly			
360	365	370	
gcc tac aat gcc ttt cag atc cgt tct gga aac aca cag ggg gac ttc			1209
Ala Tyr Asn Ala Phe Gln Ile Arg Ser Gly Asn Thr Gln Gly Asp Phe			
375	380	385	
tac att agg caa atc aac aat gtc agc gcc atg ctg gtc ctc gcc agg			1257
Tyr Ile Arg Gln Ile Asn Asn Val Ser Ala Met Leu Val Leu Ala Arg			
390	395	400	
cca gtg acg gga ccc cgg gag tac gtg ctg gac ctg gag atg gtc acc			1305
Pro Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu Met Val Thr			
405	410	415	
atg aat tcc ctt atg agc tac cgg gcc agc tct gta ctg aga ctc acg			1353
Met Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val Leu Arg Leu Thr			
420	425	430	435
gtc ttt gtg gga gcc tat acc ttc tgaagaccct caggaaaggg ccatgtgggg			1407
Val Phe Val Gly Ala Tyr Thr Phe			
440			
cccccttccc cctccatag cttaaaggc cccggggggcc tagggatgac cgttctgctt			1467
aaaggaacta tgatgtgaag gacaataaag ggagaaaagaa ggaaaa			1513

<210> 16

<211> 443

<212> PRT

<213> Artificial Sequence

<220>

<223> MBP1 murine (complete sequence)

<400> 16

Met Leu Pro Phe Ala Ser Cys Leu Pro Gly Ser Leu Leu Leu Trp Ala  
1 5 10 15

Phe Leu Leu Leu Leu Gly Ala Ala Ser Pro Gln Asp Pro Glu Glu  
20 25 30

Pro Asp Ser Tyr Thr Glu Cys Thr Asp Gly Tyr Glu Trp Asp Ala Asp  
35 40 45

Ser Gln His Cys Arg Asp Val Asn Glu Cys Leu Thr Ile Pro Glu Ala  
50 55 60

Cys Lys Gly Glu Met Lys Cys Ile Asn His Tyr Gly Gly Tyr Leu Cys  
65 70 75 80

Leu Pro Arg Ser Ala Ala Val Ile Ser Asp Leu His Gly Glu Gly Pro  
85 90 95

Pro Pro Pro Ala Ala His Ala Gln Gln Pro Asn Pr